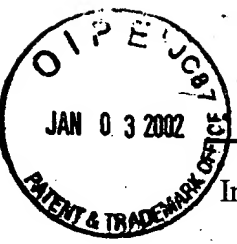


#7



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the application of: Carl H. June, *et al.*

Serial No.: 09/349,915

Filed: July 8, 1999

For: METHODS FOR SELECTIVELY
STIMULATING PROLIFERATION OF T-CELLS

Attorney Docket No.: RPI-002CP2CN1

Group Art Unit: 1636

Examiner: unknown

RECEIVED

JAN 09 2002

TECH CENTER 1600/2900

Commissioner for Patents
Box Sequence
Washington, D.C. 20231

TRANSMITTAL LETTER FOR DISKETTE CONTAINING SEQUENCE LISTING

Dear Sir:

Enclosed is a diskette which contains a computer readable form of the Sequence Listing for the above-referenced patent application. The Sequence Listing complies with the requirements of 37 C.F.R. § 1.821. The material on this diskette is identical in substance to the sequence listing appearing on pages 1-15 of the Sequence Listing which is submitted herewith, as required by 37 C.F.R. § 1.821(f). The computer readable form of the sequence listing contained on the enclosed diskette is understood to comply with the requirements of § 1.824(d).

Certificate of First Class Mailing (37 CFR 1.8(a))

I hereby certify that this correspondence is deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner for Patents, Box Sequence, Washington, DC 20231 on:

November 26, 2001
Date

Signature

Maria C. Laccotripe
Limited Recognition Under 37 C.F.R. § 10.9(b)

Respectfully submitted,

Signature

Maria C. Laccotripe, Ph.D., J.D.
Limited Recognition Under 37 C.F.R. §10.9(b)
Agent for Applicant
LAHIVE & COCKFIELD, LLP
28 State Street
Boston, MA 02109
(617) 227-7400

Date: November 26, 2001



RPI-002CP2CN1

1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: June, Carl H., Thompson, Craig B., Nabel, Gary J.
Gray, Gary S., Rennert, Paul D.
- (ii) TITLE OF INVENTION: Methods For Selectively Stimulating
Proliferation Of T-Cells
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD
 - (B) STREET: 28 State Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/349,915
 - (B) FILING DATE: July 8, 1999
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/403,253
 - (B) FILING DATE: March 10, 1995
 - (A) APPLICATION NUMBER: US 08/253,964
 - (B) FILING DATE: 3 JUNE 1994
 - (A) APPLICATION NUMBER: US 08/073,223
 - (B) FILING DATE: 4 JUNE 1993
 - (A) APPLICATION NUMBER: US 08/200,947
 - (B) FILING DATE: 23 FEB 1994
 - (A) APPLICATION NUMBER: US 07/864,805
 - (B) FILING DATE: 7 APR 1992
 - (A) APPLICATION NUMBER: US 08/247,505
 - (B) FILING DATE: 23 MAY 1994
 - (A) APPLICATION NUMBER: US 07/864,866
 - (B) FILING DATE: 7 APR 1992
 - (A) APPLICATION NUMBER: US 08/218,155
 - (B) FILING DATE: 25 MAR 1994
 - (A) APPLICATION NUMBER: US 07/864,807
 - (B) FILING DATE: 7 APR 1992
 - (A) APPLICATION NUMBER: US 07/902,467
 - (B) FILING DATE: 16 JUNE 1992
 - (A) APPLICATION NUMBER: US 07/275,433
 - (B) FILING DATE: 23 NOV 1988
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Mandragouras, Amy E.
 - (B) REGISTRATION NUMBER: 36,207
 - (C) REFERENCE/DOCKET NUMBER: RPI-002CP2
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 227-7400

(B) TELEFAX: (617) 742-4214

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B cell
- (H) CELL LINE: Raji

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA in pCDM8 vector
- (B) CLONE: B7, Raji clone #13

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: 3

(ix) FEATURE:

- (A) NAME/KEY: Open reading frame (translated region)
- (B) LOCATION: 318 to 1181 bp
- (C) IDENTIFICATION METHOD: similarity to other pattern

(ix) FEATURE:

- (A) NAME/KEY: Alternate polyadenylation signal
- (B) LOCATION: 1474 to 1479 bp
- (C) IDENTIFICATION METHOD: similarity to other pattern

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
WHITMAN, JAMES F.
NADLER, LEE M.
- (B) TITLE: B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
- (C) JOURNAL: The Journal of Immunology
- (D) VOLUME: 143
- (E) ISSUE: 8
- (F) PAGES: 2714-2722
- (G) DATE: 15-OCT-1989
- (H) RELEVANT RESIDUES In SEQ ID NO:1: FROM 1 TO 1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT   60
GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTTCT TCAGCAAGCT  120
GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT  180
GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT  240
TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTGCGCTTT CACTTTTGAC  300
CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC 353
          Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser
                    -30                               -25

AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT   401
Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu
          -20                               -15                               -10

TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA   449
Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu
          -5                               1                               5                               10

GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA   497
Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala
                    15                               20                               25

CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG   545
Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met
                    30                               35                               40

ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC   593
Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile
                    45                               50                               55

TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA   641
Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro
                    60                               65                               70

TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC   689
Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp
                    75                               80                               85                               90

GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT   737
Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala
                    95                               100                               105

GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT   785
Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn
                    110                               115                               120

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ATT AGA AGG ATA ATT TGC TCA ACC TCT GGA GGT TTT CCA GAG CCT CAC 833
 Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His
 125 130 135

CTC TCC TGG TTG GAA AAT GGA GAA GAA TTA AAT GCC ATC AAC ACA ACA 881
 Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr
 140 145 150

GTT TCC CAA GAT CCT GAA ACT GAG CTC TAT GCT GTT AGC AGC AAA CTG 929
 Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu
 155 160 165 170

GAT TTC AAT ATG ACA ACC AAC CAC AGC TTC ATG TGT CTC ATC AAG TAT 977
 Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr
 175 180 185

GGA CAT TTA AGA GTG AAT CAG ACC TTC AAC TGG AAT ACA ACC AAG CAA 1025
 Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln
 190 195 200

GAG CAT TTT CCT GAT AAC CTG CTC CCA TCC TGG GCC ATT ACC TTA ATC 1073
 Glu His Phe Pro Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile
 205 210 215

TCA GTA AAT GGA ATT TTT GTG ATA TGC TGC CTG ACC TAC TGC TTT GCC 1121
 Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala
 220 225 230

CCA AGA TGC AGA GAG AGA AGG AGG AAT GAG AGA TTG AGA AGG GAA AGT 1169
 Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser
 235 240 245 250

GTA CGC CCT GTA TAACAGTGTC CGCAGAAGCA AGGGGCTGAA AAGATCTGAA 1221
 Val Arg Pro Val

GGTAGCCTCC GTCATCTCTT CTGGGATACA TGGATCGTGG GGATCATGAG GCATTCTTCC 1281

CTTAACAAAT TTAAGCTGTT TTACCCACTA CCTCACCTTC TTAAAAACCT CTTTCAGATT 1341

AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT GCAATTTGCT 1401

TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT CTTGTCAGCC 1461

AATTCATTAT CTATTAAACA CTAATTTGAG

1491

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: B cell activation antigen; natural ligand for CD28 T cell surface antigen; transmembrane protein

(ix) FEATURE:

- (A) NAME/KEY: signal sequence
- (B) LOCATION: -34 to -1
- (C) IDENTIFICATION METHOD: amino terminal sequencing of soluble protein
- (D) OTHER INFORMATION: hydrophobic

(ix) FEATURE:

- (A) NAME/KEY: extracellular domain
- (B) LOCATION: 1 to 208
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: transmembrane domain
- (B) LOCATION: 209 to 235
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: intracellular domain
- (B) LOCATION: 236 to 254
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 19 to 21
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 55 to 57
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 64 to 66
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 152 to 154
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 173 to 175
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 177 to 179
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 192 to 194
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 198 to 200
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: Ig V-set domain
- (B) LOCATION: 1 to 104
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: Ig C-set domain
- (B) LOCATION: 105 to 202
- (C) IDENTIFICATION METHOD: similarity with known sequence

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
WHITMAN, JAMES F.

NADLER, LEE M.

(B) TITLE: B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
(C) JOURNAL: The Journal of Immunology
(D) VOLUME: 143
(E) ISSUE: 8
(F) PAGES: 2714-2722
(G) DATE: 15-OCT-1989
(H) RELEVANT RESIDUES IN SEQUENCE ID NO:2: From -26 to 262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	His	Thr	Arg	Arg	Gln	Gly	Thr	Ser	Pro	Ser	Lys	Cys	Pro	Tyr	-30	-25	-20	
Leu	Asn	Phe	Phe	Gln	Leu	Leu	Val	Leu	Ala	Gly	Leu	Ser	His	Phe	Cys	-15	-10	-5	
Ser	Gly	Val	Ile	His	Val	Thr	Lys	Glu	Val	Lys	Glu	Val	Ala	Thr	Leu	-1	1	5	10
Ser	Cys	Gly	His	Asn	Val	Ser	Val	Glu	Glu	Leu	Ala	Gln	Thr	Arg	Ile	15	20	25	30
Tyr	Trp	Gln	Lys	Glu	Lys	Lys	Met	Val	Leu	Thr	Met	Met	Ser	Gly	Asp	35	40	45	
Met	Asn	Ile	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	Ile	Phe	Asp	Ile	Thr	50	55	60	
Asn	Asn	Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg	Pro	Ser	Asp	Glu	Gly	65	70	75	
Thr	Tyr	Glu	Cys	Val	Val	Leu	Lys	Tyr	Glu	Lys	Asp	Ala	Phe	Lys	Arg	80	85	90	
Glu	His	Leu	Ala	Glu	Val	Thr	Leu	Ser	Val	Lys	Ala	Asp	Phe	Pro	Thr	95	100	105	110
Pro	Ser	Ile	Ser	Asp	Phe	Glu	Ile	Pro	Thr	Ser	Asn	Ile	Arg	Arg	Ile	115	120	125	
Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	His	Leu	Ser	Trp	Leu	130	135	140	
Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr	Val	Ser	Gln	Asp	145	150	155	
Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	Leu	Asp	Phe	Asn	Met	160	165	170	
Thr	Thr	Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	Tyr	Gly	His	Leu	Arg	175	180	185	190
Val	Asn	Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	Gln	Glu	His	Phe	Pro	195	200	205	
Asp	Asn	Leu	Leu	Pro	Ser	Trp	Ala	Ile	Thr	Leu	Ile	Ser	Val	Asn	Gly	210	215	220	

Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
 225 230 235
 Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
 240 245 250

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT 60

GAGTGGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC 115
 Met Asp Pro
 1

CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG 163
 Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu
 5 10 15

CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT 211
 Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr
 20 25 30 35

GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT 259
 Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser
 40 45 50

GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG 307
 Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu
 55 60 65

GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG 355
 Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met
 70 75 80

GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT 403
 Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn
 85 90 95

CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA 451
 Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys
 100 105 110 115

AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA 499
 Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser
 120 125 130

GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA	547
Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile	
135 140 145	
ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC	595
Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr	
150 155 160	
CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT	643
Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr	
165 170 175	
ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA	691
Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu	
180 185 190 195	
CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG	739
Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr	
200 205 210	
AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT	787
Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu	
215 220 225	
TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA	835
Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro	
230 235 240	
GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT	883
Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys	
245 250 255	
GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG	931
Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg	
260 265 270 275	
CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG	979
Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu	
280 285 290	
AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT	1027
Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser	
295 300 305	
GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC	1075
Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp	
310 315 320	
AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAA	1120
Lys Ser Asp Thr Cys Phe	
325	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Pro	Gln	Cys	Thr	Met	Gly	Leu	Ser	Asn	Ile	Leu	Phe	Val	Met	1	5	10	15
Ala	Phe	Leu	Leu	Ser	Gly	Ala	Ala	Pro	Leu	Lys	Ile	Gln	Ala	Tyr	Phe	20	25	30	
Asn	Glu	Thr	Ala	Asp	Leu	Pro	Cys	Gln	Phe	Ala	Asn	Ser	Gln	Asn	Gln	35	40	45	
Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Glu	Asn	Leu	Val	50	55	60	
Leu	Asn	Glu	Val	Tyr	Leu	Gly	Lys	Glu	Lys	Phe	Asp	Ser	Val	His	Ser	65	70	75	80
Lys	Tyr	Met	Gly	Arg	Thr	Ser	Phe	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg	85	90	95	
Leu	His	Asn	Leu	Gln	Ile	Lys	Asp	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile	100	105	110	
His	His	Lys	Lys	Pro	Thr	Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser	115	120	125	
Glu	Leu	Ser	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	130	135	140	
Ser	Asn	Ile	Thr	Glu	Asn	Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile	145	150	155	160
His	Gly	Tyr	Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	165	170	175	
Asn	Ser	Thr	Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	180	185	190	
Val	Thr	Glu	Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	195	200	205	
Asp	Val	Thr	Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	210	215	220	
Thr	Arg	Leu	Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	225	230	235	240
Pro	Pro	Pro	Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	245	250	255	
Ile	Ile	Cys	Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	260	265	270	
Lys	Lys	Arg	Pro	Arg	Asn	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	275	280	285	
Arg	Glu	Glu	Ser	Glu	Gln	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	290	295	300	
Glu	Arg	Ser	Asp	Glu	Ala	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser	305	310	315	320
Ser	Cys	Asp	Lys	Ser	Asp	Thr	Cys	Phe											

325

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /label=Xaa is any amino acid
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /label=Xaa is any amino acid
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: /label=Xaa is any amino acid
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 7
 - (D) OTHER INFORMATION: /label=Xaa is any amino acid
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 8
 - (D) OTHER INFORMATION: /label=Xaa is Asp or Glu
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 9
 - (D) OTHER INFORMATION: /label=Xaa is any amino acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Gly Xaa Trp Leu Xaa Xaa Xaa Xaa

5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 227 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro Val Lys Gly Gly Thr Lys Cys Ile Lys Tyr Leu Leu Phe Gly Phe
5 10 15

Asn Phe Ile Phe Trp Leu Ala Gly Ile Ala Val Leu Ala Ile Gly Leu

20					25					30					
Trp	Leu	Arg	Phe	Asp	Ser	Gln	Thr	Lys	Ser	Ile	Phe	Glu	Gln	Glu	Thr
	35						40					45			
Asn	Asn	Asn	Asn	Ser	Ser	Phe	Tyr	Thr	Gly	Val	Tyr	Ile	Leu	Ile	Gly
	50					55					60				
Ala	Gly	Ala	Leu	Met	Met	Leu	Val	Gly	Phe	Leu	Gly	Cys	Cys	Gly	Ala
	65					70					75				80
Val	Gln	Glu	Ser	Gln	Cys	Met	Leu	Gly	Leu	Phe	Phe	Gly	Phe	Leu	Leu
				85					90					95	
Val	Ile	Phe	Ala	Ile	Glu	Ile	Ala	Ala	Ala	Ile	Trp	Gly	Tyr	Ser	His
			100					105					110		
Lys	Asp	Glu	Val	Ile	Lys	Glu	Val	Gln	Glu	Phe	Tyr	Lys	Asp	Thr	Tyr
		115					120					125			
Asn	Lys	Leu	Lys	Thr	Lys	Asp	Glu	Pro	Gln	Arg	Glu	Thr	Leu	Lys	Ala
						135					140				
Ile	His	Tyr	Ala	Leu	Asn	Cys	Cys	Gly	Leu	Ala	Gly	Gly	Val	Glu	Gln
	145					150					155				160
Phe	Ile	Ser	Asp	Ile	Cys	Pro	Lys	Lys	Asp	Val	Leu	Glu	Thr	Phe	Thr
				165					170					175	
Val	Lys	Ser	Cys	Pro	Asp	Ala	Ile	Lys	Glu	Val	Phe	Asp	Asn	Lys	Phe
			180						185				190		
His	Ile	Ile	Gly	Ala	Val	Gly	Ile	Gly	Ile	Ala	Val	Val	Met	Ile	Phe
			195				200					205			
Gly	Met	Ile	Phe	Ser	Met	Ile	Leu	Cys	Cys	Ala	Ile	Arg	Arg	Asn	Arg
	210					215					220				
Glu	Met	Val													
	225														

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Leu Trp Leu Arg Phe Asp
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

His Gln Phe Cys Asp His Trp Gly Cys Trp Leu Leu Arg Glu Thr His
1 5 10 15

Ile Phe Thr Pro
20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Arg Leu Val Leu Glu Asp Pro Gly Ile Trp Leu Arg Pro Asp Tyr
1 5 10 15

Phe Phe Pro Ala
20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Cys Trp Leu Leu Arg Glu
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly Ile Trp Leu Arg Pro Asp

1

5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /label=Xaa is Asp or Glu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Xaa Trp Leu Xaa Xaa

1

5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTTTAGAGCA CA

12

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

RPI-002CP2CN1

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCTAAAG

8